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Result
No.
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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A70387
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C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T30807
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A;Title: Three receptor genes for plasminogen related growth factors in the genome of A;Reference number: 220880; MUID:99148833
A;Accession: T30807
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Best Local S
Matches 197
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from GB/EMBL/DDBJ

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7.0 879 2 A48575 7.0 1201 2 A35815 7.0 1201 2 B35815 7.0 2411 2 B32491 7.0 2411 2 B32491 7.0 1931 2 A59234 7.0 1931 2 A59234 7.0 1938 2 A49545 7.0 1738 2 T14867 7.0 1935 2 A59286 7.0 1935 2 T14867 7.0 1935 2 T54867 7.0 1935 2 T54867 7.0 1935 2 T54867 7.0 1935 2 T54867 6.9 1790 2 S67593 6.9 1790 2 S67593 6.9 2139 2 T14826 6.9 2139 2 T14826

ALIGNMENTS

A; Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 241 SELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLE--SPAP 121 LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSOLPEV 354 KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV 413 181 EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY 240 y Match 38.8%; Local Similarity 43.8%; hes 197; Conservative 70 61 RLYFDVGLDDSSVGDPESLQNELDRVKVNFSSKERDWREKQKAMDDLMETVELQRKALEN 120 KRPKKVPSKKMHL-----LELTKARDDMKSLQNDLTNAEKEISSLKKKVEFLQEALSTPTRTNEALGRLFFERCGAAP ESMITDMGIGQAAVEQLSIYCISLKKEYDNLKGGLKSSNEMCEKLKREVLTSNNKLHKAL LQKDVMEKEKLCSALRTQMTYLESQHNDTRAAKEEVRRLRIKMKTFESLDVVLQGQRAEV -----DSVVILLRTKYKNLVSNQGK---76; Score 925; DB 2; L Pred. No. 4.5e-42; 6; Mismatches 121; Length 433; Indels 56; 353 298 240 180 180 120 60 60 5

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centromere protein E - human N;Alternate names: centromere 312K protein; kinesin-related protein C;Species: Homo sapiens (man) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-3 C;Accession: S28261
                                                                                                RESULT
S28261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488
A;Accession: F85016
A;Status: preliminary
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-
C;Accession: F85016
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A; Residues: 1-506 <STO>
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                                                                                                                                                                                                                                                                                               -SQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVVR
                    #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:NC_001268; NID:g7267624; PIDN:CAB80936.1; GSPDB:GN00140
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21.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                               -VEKISTPPGKLEEKDGFTIQGSC----LRGREDSF
                                                                                                                                                                                                                                                        ---SLGGSVPRK-----DDLIS
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C;Geneti
A;Gene:
                                                                                                                                                                  R; Connor, R.; Churcher, C.M.;
submitted to the EMBL Data Lil
A, Reference number: Z21767
                                                            A; Residues: 1-1957 <CON>
A; Cross-references: EMBL
                                                                                                       A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                                                                                              hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C;Superfamily: centromere protein E; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide
E;7-335/Domain: kinesin motor domain homology <KMOT>
F;86-93/Region: nucleotide-binding motif A (P-loop)
E;486-2183/Domain: coiled coil #status predicted <COI>
E;486-2183/Domain: coiled coil #status predicted <COI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I. Nature 359, 536-539, 1992

A:Title: CENPF is a putative kinetochore mot A; Reference number: S28261; MUID:93024922

A:Accession: S28261

A:Molecule type: mRNA
A;Residues: 1-2663 <YEN>
A;Cross: references: EMBL:Z15005; NID:g29864;
                                      A;Cross-references: EMBL:Z70690; PID
A;Experimental source: strain 972h-;
                                                                                                                                                  A; Accession: T38077
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A;Cross-references: GDB:361164; OMIM:117143
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Best Local Similarity
Matches 93; Conserv
                    Genetics:
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SPDB:SPAC1F3.06c
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                                                                                                                                                                                               Library,
                                                                                                                                                                                               Barrell, B.G.; Rajandream,
brary, April 1996
                                          PIDN:CAA94624.1;
2h-; cosmid clf3
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Pred. No. 0.048;
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                                                               GSPDB:GN00066;
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                                                                 SPDB:SPAC1F3.06c
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330 967

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chromosomal protein XCAP-C - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
C;Accession: A55094
R;Hirano, T.; Mitchison, T.J.
Cell 79, 449-458, 1994
A;Title: A heterodimeric colled-coll protein required for mitotic chromosome A;Reference number: A55094; MUID:95042742
A;Accession: A55094
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A55094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1290 <HIR>
A;Cross-references: GB:Ul3673; NID:9563811; PIDN:AAA64679.1; PID:9563812
C;Superfamily: chromosome segregation protein SMC1
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                                                                                                                                                                                                                       QVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKK----QMKYLEQQ------
                                                                                                                                                                                                                                                                                     ---NKL------FDLAQEEENVLDREF------LKNELDNVRAQLSQKDKEKRDS
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   DQ----
                                    NQQKQMEKNLETLKKEYEKVAEKAGKVEAEVKRLHKLIVDINNHKLKAQQDKLDKVTKEI
                                                                       SAVEQLAVYCVSLKKEYENLKE-ARKASGEV-----ADKLRKDLFSSRSKLQTVYSEL
                                                                                                              QDRKAHLEEEVAKLRQATREMKNTFEKYTASLQSLSEQEVHLKAQVKELEVNVAAAAAPDK
                                                                                                                                                 QDETKQAQEEAGRLR-----SKMKTMEQIELLLQSQLPEVEEMIRDMGVGQ 191
                                                                                                                                                                                      ---VVTLQGQIIEQSGTMTGGGGKVMKGRMGSSVMVEISDDQLQKMENKLKTDTTRATEI
                                                                                                                                                                                                                                                                KGLNKIQTPENIPRLFDMVKVKDEQIKPAFYFALRDTIVANNLDQATRVAFQKDKRWR--
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   -AKLELKSAQKDLQSA----
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22.1%;
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21.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 182.5; DE Pred. No. 0.037;
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                                                                                                                                                                                                                                                                                                                                                                                                                20;
submitted to the EMBL Data
A;Reference number: Z19915
A;Accession: T24635
A;Status: preliminary; trar
A;Molecule type: DNA
                                                                                                          hypothetical protein T07C4.10a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C;Accession: T24635; S41023
                                                                                                                                                                                      RESULT
T24635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 2
A;Introns: 64/3; 99/3; 165/1; 267/3; 350/2;
C;Superfamily: RING finger homology
F;188-238/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T2
R;Henkhaus, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein B0432.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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A; Residues: 1-425
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A; Accession: T25457
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                                                                                           R; Buck,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 IRALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIINKL
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                                                                                                                                                                                                                                                                                                 DLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK 269
                                                                                                                                                                                                                                                                                                                                                                         LQSQLPEVEEMIRDMGVGQSAVEQLAVYC ----VSLKKEYENLKEARKASGEVADKLRK
                                                                                                                                                                                                                                                                                                                                                                                                              TVKSLEKKIIREKDKYRQEIPKLQATINHLTISSEETAYLKRELQESKNRLKTCEFYKIL
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                   translated
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23.0%;
                                                                                                                                                                                                                                                                                                                                    -SSEADKQLGEYLKKNGNLDTEKFFQLMKSTNK---DLTDKRRE
                                                                       Library,
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                 from
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Pred. No. 0
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Legans cosmid
                                                                       February 1995
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                                                                                                                                15-Oct-1999 #text_change
                   GB/EMBL/DDBJ
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Gaps

10;

172

294

245 62

227 354

397

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R:Yutzey, K.E.; Rhee, J.T.; Bader, D. Development 120, 871-883, 1994
A:Title: Expression of the atrial-specific myosin A:Reference number: I51302; MUID:95324374
A:Accession: I51302
                                                                                                                                                                                                                                                                                                            myosin heavy chain - chicken (fragment)
c;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
C;Accession: I51302
                                                                                                                           A;Cross-references: GB:S78540; NID:g1000404; PIDN:AAB34772.1; PID:g1000405 C;Superfamily: myosin heavy chain; myosin motor domain homology
                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-764 <YUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1138 <WIL>
A;Cross-references: EMBL:Z48055; PIDN:CAA88136.1; GSPDB:GN00021; CESP:T07C4.10a
A;Experimental source: clone T07A5
R;Berks, M.
submitted to the EMBL Data Library, January 1994
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A;Map position: 3
A;Introns: 16/1; 124/3; 146/3; 204/1; 311/3; 358/3; 615/3; 900/2;
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A;Residues: 895-1138 <BER>
A;Cross-references: EMBL:Z29443
C;Genetics:
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A; Accession: S41023
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Best Local
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RIQVGKRTIINKLFFDLA---
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                                                       Similarity
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                                      68;
                              Score 178.5; DB 2;
Pred. No. 0.032;
""smatches 127;
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-QEEENVLDR----EFLK-NELDNVRAQLSQKDKEKRD
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                                                                                                                                                                                                                                                           heavy
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                                    Indels
                                                                    Length
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                                    91;
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A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-477 <OGA>
C;Superfamily: rfp transforming protein; RING finger homology
E;12-71/Domain: RING finger homology <RNN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16
C;Accession: JE0343
В
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C; Species: Ra
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Best Local
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                                  282 PVASETVDRLVLESPAPVEVNLKLRRPSFRDDI 314
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                                                                                                                                                                                                                                                                                 71 QRNLRPNRLLTKVAEMARQHPGLHKRDL------CQIHQEPLKLFCQDDQTPICVVC
                                                                                                                                                                                                                                                                                                                    55
                                                                                                                                                                                                                                                                                                                                                      14 ATCSICLDYF---TDPVMTACGHNFCRECIQMSWEKGKGKKGKKKQKGSFPCPECREMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                        MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKL
 PVAIKTVCRV---
                                                                   GK-LQDSKASLDHQSRSLDLILLQLEEQTQQEPLQMLQDVKDTLTRKESLSMQYPEVVL-
                                                                                                                                                                                                               REAQEHRMHRVLPLDEAAREYKL----RLEEDIKYLREEMMKTETLQAKEEQTLTEWQERV 178
                                                                                                                                                                                                                                   RDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYL--EQQQDETKQAQEEAGRLRSKMKT
                                                                                                                                                                                                                                                                                                                    KRTI-INKLF---FDLAQEEENVLDREFLKNELDNVRAQLSQKDKE---KRDSQVIIDTL
                                                                                                                                                                                                                                                                                                                                                                                    ALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSR-----TCPQCRIQVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRODIDLNATFOVOTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LEDLKRQLEEEAKARNALAHALQSAQHDCDLLREQYEEEMEAKAELQRALSKANSE
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                                                                                                    RKDLFSSRSKLQTVYSELDQAKLEL--KSAQKDLQSAD--KEIMSLKKKLTMLQETLNLP
                                                                                                                                         KERRERILE----EFQKVVLFL-----VEEEPRLLQILKKEED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSADKEIMSLKKKLTMLQETL------NLPPVASETVDRLVLESPAPVEVNLKLRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHRLQNEVEDLMADVERSNAAAAALDKKQRNFDKILSEWK---QKFEESQTELEASQKEA
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-PGQIEV-LK---
                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 178; DB 2
Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-Jul-1999 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                          114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 477;
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1133 <WI2>
A; Cross-references: EMBL: 266514; PIDN: CAA91344.1;
A; Cross-references: clone K01A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1133 <WIL>
A; Cross-references: EMBL: Z34801; PIDN: CAA84332.1; GSPDB: GN00021; CESP: F59A2.6
A; Cross-references: clone F59A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F59A2.6 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC:Accession: T22976; T23157 R:Lightning, J. submitted to the EMBL Data Library, June 1994 A:Reference number: Z19645
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A; Accession: T23157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
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;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
;Accession: T22976; T23157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.4%;
Best Local Similarity 20.5%;
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492
                                                                                                                                             378
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EINVLTT-SLAEKEQQT
                                                                                                                                                                            KSHSPIQ-----DVPK--KICKGPRKESQLSL-GGQSCAGEPDEELVGAFPIFVRNAI
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                              RVRVKTVPSLFQAKLDT
                                                                                                     LGQKQPKRPRSESSCSKDVVRT---GFDGLGGRTKFIQPTDTVMIRPLPVKPKTK--VKQ 448
                                                                                                                                          EKHTGIQRAQGALDDAEKEVKVLKEQLERAQSALESSQELASSQKADKIQELEKELQNA-
                                                                                                                                                                                                                                                   ASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLE
                                                                                                                                                                                                                                                                                        SSAISEITKQMEAAKKELEASEKEKSELREQMDRLQKVHNAGQEDIQKLQKTWELEMAKI
                                                                                                                                                                                                                                                                                                                 -SELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET-----
                                                                                                                                                                                                                                                                                                                                                                 LLLESTTSEMKQHAEAAEIVKKQ---LEEAQSS----IENLKKDAENERN-LKTALESDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEQQQDETKQAQEEAGRLRSKMKTM------EQIELLLQSQLPEVEEMIRDMGVGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSQKDKEKRDS-QVIIDTLRDTLEERNATVVS-----LQQALGKAEMLCSTLKKQMKY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102;
                                                                   -----QKRSSEELETANEMVRSLTATLENSNSETEILKQKLETLDKELQARQQTEKALTE
                                                                                                                                                                                                                                                                                                                                                                                                 -SAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY----
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                                  465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169;
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A;Status: preliminary; nucleic acid sequence n
A;Molecule type: DNA
A;Residues: 1-1156 <AQE>
A;Cross·references: GB:AE000699; NID:g2983238;
A;Experimental source: strain VF5
C;Genetics:
A;Gene: xcpC
C;Superfamily: chromosome segregation protein
                                                                                                                                                                                                                                                                                                         chromosome assembly protein homolog - /
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                    RESULT
B70356
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A;Molecule type: DNA
A;Residues: 1-1156 <KLE>
A;Cross-references: GB:AE000995; GB:AE000782; NID:92689;
C;Superfamily: chromosome segregation protein SMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Tittle: The complete genome sequence of the hyperthermophilic, sulfate-reducin A; Reference number: A69250; MUID:98049343
A; Accession: E69444
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
C;Accession: E69444
                                                                                                                                                                 A;Title: The complete genome A;Reference number: A70300; NA;Accession: B70356
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E69444
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R;Deckert, G.; Warre
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                                                                                                                                                                                                                              Nature 392,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---STFGDVNLKAIQEYEEVKARRDELVE---KKMVLEKERADILD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQ
                                                                                                                                                                                                                              353-358,
                                                                                                                                                                                                                                                                      Warren, P.V.;
                                                                                                                                                                                                                              1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%;
21.4%;
                                                                                                                                                                                      e of the hyperthermophilic MUID:98196666
                                                                                                                                                                                                                                                                      Gaasterland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 0.068;
89; Mismatches 116;
                                                                                   NID: g2983238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 176.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VEVPENLPPL -- EKVEK -VLD-
                                                                                                                                                                                                                                                                                                                                                 Aquifex aeolicus
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SMC1
                                                                                                                                                                                                                                                                  Young, W.G.;
                                                                                      PIDN: AAC06839.1;
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                                                                                                                                              shown;
                                                                                                                                                                                                         bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      998
                                                                                                                                                                                                                                                                      Lenox,
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                                                                                      PID:g2983243;
                                                                                                                                                                                                         Aquifex
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                                                                                                                                                                                                                                                                    A.L.;
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C; Superfamily: myosin heavy chain; myosin motor domain homology C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated F; 92-775/Domain: myosin motor domain homology <a href="Monology chyoty: F: 182-189/Region: actin binding #status predicted F: 644-576/Region: actin binding #status predicted F: 648-1227/Domain: coiled coil #status predicted <a href="Monology chyoty: F: 1288-1247/Domain: chinge chin">Monology chyoty: F: 1288-1227/Domain: coiled coil #status predicted coil #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin heavy chain II - Acanthamoeba castellanii
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Acanthamoeba castellanii
C;Date: 31-Dec1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: A27224
R;Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
J. Cell Biol. 105, 913-925, 1987
J. Cell Biol. 105, 913-925, 1987
A;Reference nucleotide sequence and deduced polypeptide sequence of a A;Reference number: A27224; MUID:87308395
A;Accession: A27224
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C;Genetics:
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A27224
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A; Residues: 1-1509 < HAM>
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        102 VIIDTLRDTLEERNATVVSLQQALGKAE-----
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                                                                                                              60 NKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPVEVNLKLRRPSFRDDIDL-NATFDVDTPPARPS----SSQHGYYEKLCLE---KSHS
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                                                                                                                                                                  97; Conservative
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                                                                                                                                                             7.4%; Score 176; DB 1; Length 1509;
23.4%; Pred. No. 0.099;
tive 74; Mismatches 156; Indels &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 176; DB 2; Length 1156; 22.0%; Pred. No. 0.072;
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-MLCSTLKKQMKYLEQQQD 147
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A; Nolecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1690 <LAN>
A; Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A; Cross-references: Extain Oregon R
                                                                                                                                                                                            A;Title: A class VI unconventional myosin A;Reference number: 217588; MUID:98139549 A;Accession: T13030
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R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
                                                                                                                                                                                                                                                                                                                                                                                     microtubule binding protein D-CLIP-190 - fruit fly C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
                                                                                                                                                              A; Status: preliminary; translated
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1009 SKADAWSQEMLQKEKELQELRQQLQDSQDSQTKLKAEGERKEKSFEES---IKNLQEEVT 1065 835 QVQLEQLQQQAAASGEEGSKTVAKLHDEISQLKSQAEETQSELKSTESNLEAKSKQLEAA 210 --NLKEARKASGEVAD---KLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEI 167 E-QIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYE-------108 RDTLEERNATVVSLQQALGKAEMLCSTLKKQMK-YLEQQQDETKQAQEEAGRLRSKMKTM 166 724 QIQLEKESIEQQL--ALKQNELEDFQKKQSESEVHLQEIKAQNTQKDLELVESGESLKKL 50 RIQVGKRTIINKLFFDLAQEEENVLDREFLKNE--LDNVRAQLSQKDKEKRDSQVIIDTL 107 QQQLEEKTLGHEKLQAAL-----EELKKEKETIIKEKEQELQQLQSKSAESESALKVV NGSLEEEAKKSGQLQEQITKLKSEVEETQAALSSYHTDVESKTKQLEAANAALEKVNKEY MSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVN--LKLRRPSFRDDI-----DLN 317 Conservative 7.3%; 20.9%; -KEITDTLHAELQAERSSSSALHTKLSKFSDEIATGHKELT 84; Mismatches Score 175; DB Pred. No. 0.13; DTPPARPSSSOHGYYEKLCLEKSHSPIODVPKKIC 357 DB 2; 157; Length 1690; Indels Gaps 1008 264 954 894 209 781 13;

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A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-1938 <MAE>
A;Residues: 1-1938 <MAE>
A;Cross-references: GB:G32574; NID:g940232; PIDN:AAA74199.1; PID:g940233 A;Experimental source: strain New Zealand White; cell type skeletal muscl C;Genetics: A;Gene: MHC C;Genetics: A;Gene: MHC C;Superfamily: myosin heavy chain; myosin motor domain homology F;89-769/Domain: myosin motor domain homology <MMO>
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                                                                                            myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum) (Contains: myosin ATPase (EC 3.6.1.32) (Species: Dictyostelium discoideum C;Species: Dictyostelium discoideum C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-C;Accession: A26655; A24728; S00250 R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
A;Title: Conserved protein domains in a myosin A;Reference number: A26655; MUID:87092266 A;Accession: A26655 A;Molecule type: DNA
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R;Wagle, G; Neegel, A.; Scheel, J.; Gerisch, G.
FEBS Lett. 227, 71-75, 1988
A;Title: Phosphorylation of threonine residues on cloned fragments of t
A;Reference number: $00250; MUID:88112226
A;Accession: $00250
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1734-1893 <WAG>
C;Comment: The rod domain is highly periodic, containing a pattern of 7
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide bind
F;19-186/Region: nucleotide-binding motif A (P-loop)
F;819-2116/Domain: alpha-helical rod <ROD>
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S21801
                       R;Sun, W.; Chantler, P.D. Biochem. Biophys. Res. Co
                                                                                       A; Molecule type: mRNA
A; Residues: 1-1999 <SUN>
                                                                                                                                                      J. Mol. Biol. 224, 1185-1193, 1992
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the cDNA encoding a napresering and a control of the cDNA encoding and a control of the cDNA encoding and a control of the cDNA en
                                                                                                                                                                                                                                             C; Accession: S21801; pN0013; S18134
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N;Alternate names: myosin II
N;Contains: myosin ATPase (EC 3.6.1.32)
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A; Residues: 2035-2116 <DEL>
                                                                    A; Cross references: EMBL: X62659
                                                                                                                                 A; Accession: S21801
                                                                                                                                                                                                                                                                                            C; Species: Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDV 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLEKSLKDTESNVLDLQRQLKAEKETLKAMYDSKDALEAQKRELEIRVEDMESELDEKK 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKKICKGPRKESQLSLGGQSCAGEPDEE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEA----ANKKLQ----GEYTELNEKFNSEV-TARSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVRLQ----SELDDLTVRLDSETKDKSELLRQKKKLEEELKQVQEAL-----AAETAAKLA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEEELEEMKR-VNDGQSDTISRLEKIKDELQKEVEELTES--FSEESKDKGVLEK----T
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Res. Commun. 175, 244-249, 199 cellular myosin II exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESQL----VAVNNELDEE 1106
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27.48;
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on 31-Dec-1993
                                                                                                                                                                                neuronal
                            1991
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A;Reference number: PN0013; MUID:91151356
A;Accession: PN0013
A;Residues: 1914-1998,'I' <SU2>
A;Experimental source: brain
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Reywords: actin binding; ATP; coiled coil; hydrolase; methylated amino a
F;84-763/Domain: myosin motor domain homology <MMOT>
F;84-763/Domain: myosin motor domain homology <MMOT>
F;141-181/Region: nucleotide-binding motif A (P-loop)
F;415-75/Region: actin binding #status predicted
F;836-125/Region: actin binding #status predicted
F;836-1276/Region: coiled coil #status predicted
F;1277-1999/Region: 1ight meromyosin
F;127/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                RESULT 18

$54871

M protein - Streptococcus sp.
C;Species: Streptococcus sp.
C;Cate: 08-Jul-1995 #sequence_revision 21-Jul-19
C;Accession: $54871
R;Podbielski, A.; Melzer, B.
submitted to the EMBL Data Library, June 1991
A;Reference number: $54871
A;Accession: $54871
A;Molecule type: DNA A;Residues: 1-532 <POD>
A;Residues: 1-532 <POD>
A;Cross references: EMBL:X60097; NID:g840905; PIDN:CAA42693.1; PID:g840906 C;Superfamily: M5 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 DKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQM-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKKMEDSVGCLETAEEVKRKLQKDLEGLS----QRHEEKVAAYDKLEKTKTRLQQELDDLL 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PKRPRSESSCSKDVVRTGFDGL 420
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18.7%; Pred. No. 0.24;
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                                                                                                                                                                                                                                                        21-Jul-1995 #text_change 26-Aug-1999
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	Query Match 7.1%; Score 170; DB 2; Length 532; Best Local Similarity 21.5%; Pred. No. 0.059; Matches 82; Conservative 67; Mismatches 141; Indels 92; Gaps 12;
eotid	Qy 55 KRTIINKLFFDLAQEEENVLDREFLKNELDNVRAQ 89 :: : :
	Oy 90 LSOKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKK 137
	Db 219 LNIDNIDLKHELEQEKQKAEADROT-LEAEKAKLEEEKQISDASRQSLRRDLDASREAKK 277
	Qy 138 QMKYLEQQQDETKQAQEEAGR-LRSKMKTMEQIELLLQSQLPEVEEMIR 185
	Db 278 QLEAEYQKLEEEKQISDASRQSLRRDLDASREAKKQLEAEYQKLEEQNKISEASRKGLRR 337
	186 DMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQ
	DD 338 DLDASKEAKKQYEKDLANLTAELDKYKEEKQISDASKKGLRKDLDASKE 386
	QY 246 AKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKL 305
	EANSKLAALEKLNKELEESKKLTEKEKAELQAK
	Qy 306 RRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKK 355
	Db 433 EAKALKEKLAKQAEELAKLRAGKASDSQTPEATPGNKVVPGKGQAPQAGTKPN 485
	Qy 356 ICKGPRKESQLSLGGQSCAGEP 377
	Db 486 QNKEPMKETKRQLPSTGEATNP 507
	RESULT 19 A70387 conserved hypothetical protein aq_1006 - Aquifex aeolicus
	C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Feb-2001
	R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.
	Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
	ID: 98196666
	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-978 <aof></aof>
	A;Cross-references: GB:AE000718; NID:92983504; PIDN:AAC07092.1; PID:92983515; GB:A A;Experimental source: strain VF5 C;Genetics:
	A;Gene: aq_1006 C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
	Query Match 7.1%; Score 170; DB 2; Length 978; Best Local Similarity 22.6%; Pred. No. 0.12; Matches 79; Conservative 70; Mismatches 125; Indels 76; Gaps 13;
	Qy 41 APSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREFLKNE 82
	VCGGIYRGKALENVDAEGISELKHAKELK
	RDSQVIIDTLRDTLEERNAT : : :
	Db 541 MEKLRNEVEELRKEIPENLKERIKKLEELRIEKEKLEHKLNKYRKAL 587
. <u>—</u> .	143 EQQQDETKQAQEEAGRURSKMKTMEQIELLLQSQL-PEVEEMIRDMGVGQSAVEQLAVYC
_	ON DUTCHOOK DISPONDED TO THE FOREST CONTRACTOR OF THE STATE OF THE STA

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myosin heavy chain, skeletal muscle, embryonic - rat

N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Rattus norregicus (Norway rat)
C;Date: 31-Dec.1993 #sequence_revision 31-Dec.1993 #text_change 19-Jan-2001
C;Accession: A24922; A2538; B24263
R;Strehler, E.E.; Strehler-Page, M.A.; Perriard, J.C.; Periasamy, M.; Nadal-Gin:
J. Mol. Biol. 190, 291-317, 1986
A;Fitle: Complete nucleotide and encoded amino acid sequence of a mammalian myo:
A;Reference number: A24922; MUID:87060988
A;Accession: A24922
A;Molecule type: DNA
A;Residues: 1-1940 <STR>
A;Cross-references: GB:X04267; GB:X05004; NID:g56658; PIDN:CAA27817.1; PID:g161-
A;Fitle: Intron positions are conserved in the 5' end region of myosin heavy-ch:
A;Reference number: A22538; MUID:85080119
A;Accession: A22538; MUID:85080119
A;Accession: A22538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change
C;Accession: JH0720
R;Hemmati-Brivanlou, A.; Mann, R.W.; Harland, R.M.
Neuron 9, 417-428, 1992
A;Title: A protein expressed in the growth cones of embryonic ve
A;Reference number: JH0720; MUID:92398961
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A;Molecule type: mRNA
A;Molecule: 1-1744 <HEM>
A;Cross-references: GB:M99387; NID:g214816; PIDN:AAA49966.1; PID:g214817
A;Experimental source: tadpole head
C;Keywords: intermediate filament
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEYKSEVSVLEAGLSESKENLRKVLEENKQNRLLLQSLDKELVSLKMRKEALEDLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAEMVRDSIYEEIEFVKQRCLEEKQAREDAKKELSESKKLLEEETRAQIWLKERLGQLEA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SADKEIMSLKKKLIMLQETLNLPPVASETVDRLVLESPAPVE----
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25.7%;
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Pred. No. 0.26;
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                                                       heavy-chain
                                                                                                                      PID:g1619328
                                                                                                                                                                                                                                           myosin
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A; Variety: group G C; Date: 07-Sep-1994 #sequence_revision C; Accession: \$45599; \$43554 Rinadahl.

plasminogen-binding protein MLG72 C; Species: Streptococcus sn.

Streptococcus

sp.

03-Nov-1995 #text_change Sjoebring, bound

22

R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Eur. J. Biochem. 222, 267-276, 1994

A; Reference number: S45598; MUID: 94291620

activates

plasminogen

ţo

group a

and

A; Title: Streptokinase

A; Molecule type: I A; Residues: 1-472

A; Status: preliminary A; Accession: S45599

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A;Introns: 68/3; 116/3; 169/1
A;Note: the list of intron positions may be incomplete C;Superfamily: myosin heavy chain; myosin motor domain t C;Keywords: actin binding; ATP; coiled coil; hydrolase; F;89-767/Domain: myosin motor domain homology <MMOT>F;179-186/Region: nucleotide-binding motif A (P-loop) F;549-586/Region: actin binding #status predicted F;656-678/Region: actin binding #status predicted F;840-1940/Domain: coiled coil #status predicted F;840-180/Region: S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1358-1490,'G' <PER>
A;Cross-references: GB:K03468; NID:9205573; PIDN:AAA41652.1; PID:9205574
A;Experimental source: clone pMHC-72
C;Genetics:
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F;130/Modified site: N6,N6-trimethyllysine (Lys)
F;185/Binding site: ATP (Lys) #status predicted
F;696,706/Active site: Cys #status predicted
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A;Cross-references: GB:
Вb
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1415 LEKT 1418
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                                                 274 LQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 DHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVL 74
                                                                                                                                                                                                IVSQLSRSKQAFTQQIEELKRQLEEENKAKNALAHALQSSRHDCDLLREQYEEEQEGKAE 1357
                                                                                                                                                                                                                                                                                                                                               SLQQALGKAEMLCSTLKKQMKYLEQQQDETKQA-----
                                                                                                                                                                                                                                                                                                                                                                                                 QHEATVATLRKKHADSAAELAEQIDNLQRVKQKLEKEKSEFKLEIDDLSSSVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYARE-----LEELSERLEEAGGVTSTQIELNKKREAEFLKLRRDL---EEATL 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary
                                                                                                LQRALSKANSEVAQWRTKYETDAIQRTEELEEAKKKL--AQR-LQDSEEQVEAVNAKCAS 1414
                                                                                                                          SGEVADKLRKDLFSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTM
                                                                                                                                                                                                                                                                                              SVSKSKANLEKICRTLEDQLSEARGKNEETQRSLSELTTQKSRLQTEAGELSRQLEEKES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%;
23.0%;
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Pred. No. 0.3;
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A; Molecule type: mRNA
A; Residues: 1-1935 < KRA>
A; Residues: 1-1935 < KRA>
A; Residues: 1-1935 < KRAP
A; Cross references: EMBL:X15939; NID:g56656; PIDN:CR; McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Tayly J. Mol. Biol. 210, 665-671, 1989
A; Title: Full-length rat alpha and beta cardiac myc A; Reference number: S07535; MUID:90133919
A; Reference number: S07535; MUID:90133919
A; Recession: S07536
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-950, 'RK', 953-1935 < MCN>
R; Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-R; Title: Cardiac myosin heavy chain isozymic trans; A; Reference number: I53305; MUID:85179510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin beta heavy chain, cardiac muscle [similarity] - rat N;Contains: myosin ArPase (EC 3.6.1.32) C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change C;Accession: 506006; S07536; I67441; A02989 R;Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A. Nucleic Acids Res. 17, 7529-7530, 1989 A;Title: Complete nucleotide sequence of full length cDNA for ra
                     A;Cross-references: GB:M32698; NID:g205598; PIDN:AAA41659.1; R;Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B. Nature 297, 659-664, 1982
                                                                                A;Accession: 167441
A;Status: translated from Gl
A;Molecule type: mRNA
A;Residues: 1871-1935 <RES>
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  A; Title: Molecular characterization
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                                                                                                                                                                                                                                                                                                                                                             chain
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genes expressed
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                                                                                                                                                                                      development and
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1310

65 DLAQEEENVLDREFLKN---ELDNVRAQLSQKDKEKR------DSQVIIDTLRDTLEER 114

ELESSQLKIADLEHLKTLQPELETLQKHVGQKEEEEVSYLVGQLGEKEQTLTTVQTEMEEQ 1369

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A; Residues: 1524-1528, 'V',1530,'R',1532-1730,'H',1732-1783,'K',1785-1850,'N',1852-185
A; Cross-references: GB.400752; NID:9205577; PIDN.AAA41654.1; PID:9205578
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
C; Keywords: myosin motor domain homology cMMOT>
F; 88-766/Domain: myosin motor domain homology cMMOT>
F; 178-185/Region: actin binding #status predicted
F; 955-677/Region: actin binding #status predicted
F; 955-677/Region: actin binding #status predicted
                                                                                                                           A;Cross-references: DDBJ:D25543; NID:g516825; PIDN:BAA05026.1; PID:g516826 C;Comment: This protein plays a role in the formation and maintenance of the characte C;Superfamily: giantin rg:49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status pred F;3165-3187/Domain: membrane anchor #status predicted <MAD>
                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-3187 <TOK>
                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: JC5837
                                                                                                                                                                                                                                                                                                                                                                  R;Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Cell Struct. Funct. 22, 565-577, 1997
A;Title: Identification and characterization of rat 364-kDa Golgi-asse A;Reference number: JC5837; MUID:98093490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364K Golgi complex-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar.1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: JC5837
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F:129/Modified site: N6.N6.N6-trimethyllysine (Lys)
F:184/Binding site: ATP (Lys) #status predicted
F:695,705/Active site: Cys #status predicted
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A; Residues: 1524-1528
                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown
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                             Query Match
Best Local :
     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSKLQT - - - - VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKQMKYLEQQQDETKQAQEEAGRLRSKMKT-----MEQIELLLQSQLP-----
  Similarity 19.89; Conservative
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                        7.18;
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22.5%;
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Score 168.5;
Pred. No. 0.61
34; Mismatches
                             . 61;
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.32;
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     160;
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     127;
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transcytosis-associated protein pl15 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C;Accession: A55913
R;Barroso, M.; Nelson, D.S.; Sztul, E.
Proc. Natl. Acad. Sci. U.S.A. 92, 527-531, 1995
A;Title: Transcytosis-associated protein (TAP)/pl15 is a general fusion fact A;Reference number: A55913; MUID:95132633
A;Accession: A55913
A;Status: preliminary
A;Status: preliminary
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C;Keywords: membrane fusion;
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             δÃ
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A; Residues: 1-959 <BAR>
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                                                                                                                                                             AVTQQASQTQQHKDQYNLLKVQLGKDNHHQGSHSDGAQVNGTQPEEISRLREEIEELRSH
                                                                                                                                                                                                                       SSEEDKKEEEV-----KKTLEQHDNIVTHYKNVIREQDLQLEELKQQVSTLKCQNEQLQT
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             ASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKD-
                                                                                                     QVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAEQVAELKQELSALKSQLCSQS
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                                                                                                                                   ELLLQSQLPEVEEMIRDM-----
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                                            LEITRLQTENRELQQRAETLAKSVPVEGESELVTAAKTTDVEGRLSALLQETKELKNEIK
                                                                                                                                                                                               --TKQAQ---
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                                                                                                                                                                                                                                                                                                                                             76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     membrane
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Pred. No. 0.15
56; Mismatches
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             A;Description: supposed to play some role C;Keywords: leucine zipper
                                                                                                                                                                         R; Kondo, M.; Sutou, S.
DNA Seq. 7, 71-82, 1997
                                                                                                                                                                                                                                                                                                                             В
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A; Introns: 15/3;
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62; Conser
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hypothetical protein T10G3.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc;Accession: T24806 R;Burton, J. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19937
                                        A; Molecule type: mRNA
A; Residues: 1-1325 <KON>
A; Cross-references: EMBL: D78270; NID:d1096175;
A; Experimental source: strain CD-1
                                                                                                                                                A; Title: Cloning and molecular characterization A; Reference number: Z22242; MUID:97217683 A; Accession: T42722
                                                                                                                                                                                                                                                                           male-enhanced antigen-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision
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for spermatogenesis
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                                                              PID:d1020389;
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915

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343

865

289

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hypothetical protein KIAA0477 - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.C.Species: Homo sapiens (man)
C.C.Species: T00259
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, N.; Nakajima, D.; Nomura, N.;
R.Seki, N.; Ohira, M.; Nakajima, N.; Nakajima, N.;
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Matches 77
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Best Local Similarity 22.8%;
Matches 91; Conservative 8
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                                                                                                                                                                                                                                                                                   601 HLNHSLSHKEQLLQEF-----RELLQYRDNSDKTLEANEML--LEKLRQRIHDKAVALER
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                                                                                                                                                                                                                                                                                                                                      24 HCGHTF-HLQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF-LKN
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                                                                                                           LCSTLKKQMKYLEQQQDETK----QAQEEAGRLRSKMKTMEQIELLLQSQLPEVEE----
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                          MIRDMGVGQSAV-EQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSK---
                                                                        L-STTCQNLQWLKEEM-ETKFSRWQKEQES-----IIQQLQTSLHDRNKEVEDLSAT
                                                                                                                                                                               AIDEKFSALEEKEKELRQLRLAVRERDHDLERLRDVLSSNEATMQSMESLLRAKGLEVEQ
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                                                                                                                                                                                                                                                                                                                                                                                       b; Score 167.5;
b; Pred. No. 0.2;
82; Mismatches
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A; Introns: 6/2;
A; Note: F5E19_70
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A; Residues: 1-853 <SAT>
A; Cross-references: EMBL:AL391147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z25394
A; Accession: T51505
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Best Local Similarity
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                                                   EVIF
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                                                                                                                                                                                                    KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV
                                                                                                                                                                                                                                                          ENGELSES--EKDYDL-----LPKVVEFSSENGH--RSVEEKSAKVETLDHEPPQE--
                                                                                                                                                                                                                                                                                                        VNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKS-----HSPIQDVP 353
                                                                                                                                                                                                                                                                                                                                                              EAKAESMKLKENLLDKETEFQNVIHENEDLKAKEDVSLKKIEELSKLLEEAILAKKQPEE
                                                                                                                                                                                                                                                                                                                                                                                                               SADKEIMSLKKKL------TMLQETLNLPPV--ASETVDRLVLESPAPVE 300
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21.9%; Pred. No. 0.15;
vative 80; Mismatches 141;
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Sequence Database,
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August 2000
                                                                                                                                                       -KPEVETEKKEKKDESQDDDKDDSV
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Gaps

19;

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214

165

613 258

673

763

720

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A;Title: Molecular cloning and pre-mkNA maturation of Onchocerca A;Reference number: A48575; MUID:93165084
A;Recession: A48575
A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Molecule type: mkNA
A;Molecule type: mkNA
A;Residues: 1-879 < CAHD-
A;Note: sequence extracted from NCBI backbone (NCBIP:125109)
C;Superfamily: myosin heavy chain; myosin motor domain homology
                                                         R:Collier, V.L.; Kronert, W.A.; O'Donnell, Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions :
A;Reference number: A35815; MUID:90346288
A;Accession: A35815
                                                                                                                                                            myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment) (Species: Drosophila melanogaster C;Date: 12-Oct-1990 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000 C;Accession: A35815
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A35815
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C;Speciles: Onchocerca volvulus
C;Speciles: Onchocerca volvulus
C;Date: Ol-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Jun-1998
C;Accession: A48575
R;Dahmen, A.; Gallin, M.; Schumacher, M.; Erttmann, K.D.
Mol. Blochem. Parasitol. 57, 335-338, 1993
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;Molecule type: DNA :Residues: 1-1201 <COL>
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Local Similarity 19.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DSQVIIDTLRDTLEERNATVVSLQQALGKA----
                                                                                                                                                                                                                                                                                                                       ----GRI----TDLVSIN----NNLTAIKN--KLETELSTAQADLD
                                                                                                                                                                                                                                                                                                                                                          RTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQAKLD
                                                                                                                                                                                                                                                                                                                                                                                                     DQYALAQRKVSALSAELEEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEIARLKKKYQAEIAELEMTVDNLNRANIEAQKTIKKQSEQLKVLQASLEDTQRQLQQTL
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Pred. No. 0.16;
8; Mismatches 160
                                                                                                                                                                                                                                                                                                                                                                                                 ----KVALDNAIRARKQAEIDLEEAN---
                                                                                                     are
                                                                                                                                        P.T.; Edwards,
                                                                                                     utilized
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                                                                                                                                        K.A.; Bernstein,
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                                                                                                  tissue-specific
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A;Cross-references: EMB
A;Note: the authors tra
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: Fly
C;Superfamily: myosin h
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                   RESULT
B35815
                  A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myos
                                                                                 A;Molecule type: DNA
A;Residues: 1-1201 <COL>
A;Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37311.1;
A;Note: the authors translated the codon TGC for residue 649
                                                                                                                                                                          A;Title: Alternative myosin hinge regions A;Reference number: A35815; MUID:90346288 A;Accession: B35815
                                                                                                                                                                                                                                                                myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000 C;Accession: B35815
                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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; Keywords:
                                                                     ;Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       32
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                                                                                                                                                                                                                                                                                                                                                                                                                                         LGQKQPKRPRSESSCSKDVVRTGFDGLGGRTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKICKGPR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQTQEKLRKALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEQEENKVLRAQL ---ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG 845
                                                                                                                                                                                                                                                                                                                                                                                                          VGRGASPAPRATS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKLQQKIKTYKRQIEEAEEIAALNLAKFRKAQQELEEAEERADLAEQAISKFRAKGRAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R--EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----ELADAHEQLNEVSAQ
                                                                                                                                                                                                                        v.L.; Kronert, W.A.; O'Donnell, P.T.;
4, 885-895, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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in heavy chain; myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:X53155; NID:g8219; PIDN:CAA37310.1; PID:g2546938 translated the codon TGC for residue 649 as Lys, and
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20.5%;
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Pred.
                   myosin motor
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No. 0.
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                                                                                                                                                                                                               utilized
                   domain
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                                                                                                                                                                                                                                            Edwards, K.A.; Bernstein,
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                                                                                        PID:g2546939
as Lys, and
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                                                                                       Lys,
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Query Match
Best Local Similarity
Matches 93; Conserv

Conservative

76;

Mismatches

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7.0%;

Score 167; Pred. No. 0

DB 2; .23;

Length 1201;

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Q
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c:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; nucleotide binding: P-loop
F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>
F:227-234/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rigeorge, E.L.; Ober, M.B.; Emerson Jr., C.P. Mol. Cell. Biol. 9, 2957-2974, 1989
A;Title: Functional domains of the Drosophila A; Reference number: A32491; MUID:89384556
A;Accession: B32491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 33
B32491
B32491
myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Species: 12-Cct-1999 #sequence_revision 31-Dec-1993 #text_change 02
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                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA; mRNA
A; Residues: 1-2411 <GEO>
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                                                                                                                                                    66 LAQEEENVLDREFLKNELDNVRAQLSQKDKEK-----RDSQVIIDTLRDTLE----
                                                                                                                                                                                                                Local Similarity
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                               KTMEQIEL - - - - - LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA
                                                              KAEALRMKKKLEADINELEIALDHANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDA
                                                                                                                               LEQEENKVLRAQL----ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGRGASPAPRATS-----VRPQFDGLAFPPRF 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGQKQPKRPRSESSCSKDVVRTGFDGLGGRTKF 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQKNLRKSERRVKELSFQSEED - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NASISAAKRK----LESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R--EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----ELADAHEQLNEVSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTMEQIEL------LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAEALRMKKKLEADINELEIALDHANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAQEEENVLDREFLKNELDNVRAQLSQKDKEK-----RDSQVIIDTLRDTLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQSADKEIMSLKKKLTMLQETLNLPPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEQEENKVLRAQL---ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG
·EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----ELADAHEQLNEVSAQ
                                                                                                                                                                                                  Conservative
                                                                                              -ERNATVVSLQQALGKAEMLCSTLKKOMKYLEQQQDETKQAQEEAGRLRSKM
                                                                                                                                                                                                                7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  GB:M27194
the codon
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                                                                                                                                                                                                 76;
                                                                                                                                                                                                              Score 167; DB 2; Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                   codon
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   TGC
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                                                                                                                                                                                                                                                                                                                                                                                                   for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melanogaster muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AKL--ELKSAQKD
                                                                                                                                                                                                 144;
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                                                                                                                                                                                                                                Length 2411;
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C;Accession: C96667

C;Accession: C9667

C;Accession: C9667

C;Accession: C9667

C;Accession: C96667

C;Accession: C9667

C;A
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A; Map position:
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C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-555 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005173; NID:g10645401; PIDN:AAG21519.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 02-Mar-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2377 VGRGASPAPRATS-----VRPQFDGLAFPPRF 2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2224
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                                                                                   77
                                                                                                                                                                                                                                                      22 AIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIINKLF---FDLAQEEENVLDR--
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F15H21.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, 71502-69704 [imported] - Arabidopsis thaliana
es: Arabidopsis thaliana (mouse-ear cress)
02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
                                                                               EFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNA------TVVSLQ
                                                                                                                                                                       AVESEHQEILKKLKESDE-----ICGNLRVETEKLTSENKELNEKLEVAGETESDLNQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKNLRKSERRVKELSFQSEED-
EDVKKERDGLEAELASKAKDHESTLEEVNRLQGQKNETEAELEREKQEKPALLNQINDVQ
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                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                            7.08;
                                                                                                                                                                                                                                                                                                                                              75;
                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.09
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Score 166.5; DB
Pred. No. 0.095;
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                                                                                                                                                                                                                                                                                                                                              173;
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                                                                                                                                                                                                                                                                                                                                     77;
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123 QALGKAEMLCSTLKKOMKYL----EQQQ------DETKQAQEEAGRLRSKMKTMEQIEL 171

KALLEQEAAYNTLSQEHKQINGLFEEREATIKKLTDDYKQAREMLEEYMSKMEETER---

LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFS

231

321

374

RMQETGKDVASRESAIVDLEETVESLRNEVERKGDEIESLMEKMSNIEVKLRL

SNQKLRVTEQVLTEKEGELKRIEAKHLE----

EQALLEEKIATTHETYRGLIKEISERVD

SRSKLQTVYSELDQAKLELKSAQ-KDLQSADKEIMSLKKKLTMLQETL-NLPPVASETVD 289

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RESULT 35
A59234
Slow myosin heavy chain 3 - quail
C;Species: Coturnix coturnix
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C;Accession: A59234
R;Nikovits Jr., W; Wang, G.F.; Feldman, J.L.; Miller, J.B.; Wade, R.; Nelson, L.
J. Biol. Chem. 271, 17047-17056, 1996
A;Title: Isolation and characterization of an avian slow myosin heavy chain gene
A;Reference number: A59234; MUID:96291845
A;Accession: A59234
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1931 <NIK>
A;Cross-references: GB:U53862; NID:91289513; PIDN:AAC59912.1; PID:91289514
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;81-761/Domain: myosin motor domain homology
                                                                                                                                                 RESULT 36
A49345
A49345
A49345
A49345
A49345
A49345
A79345
A;Accession: A49545
A;Molecule type: DNA
A;Residues: 1-388 <BE
A;Cross-references: E:
R;Whatmore, A.; Kapur
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   Cross-references: EMBL:Z22219; NID:Whatmore, A.; Kapur, V.; Sullivan,
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Best Local :
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NID:g288978;
van, D.; Musse
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Pred. No. 0.43;
4; Mismatches
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3978; PIDN:CAA80222.1; Musser, J.; Kehoe, M.
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ke protein (Pd
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RESULT
S46489
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A;Experimental source: serotype M53
A;Experimental source: serotype M53
R;Carlsson Wistedt, A; Ringdahl, U.; Mueller-Esterl, W
Mol. Microbiol. 18, 569-578, 1995
A;Title: Identification of a plasminogen-binding motif
A;Reference number: S70457; MUID:96342385
A;Accession: S70459
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A; Residues: 30-162 < CAR>
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A; Residues: 17-77 < WHW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U11975; NID:g533627; PIDN:AAA99591.1; A;Experimental source: serotype M53
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A;Description: Noncongruent relationships between variation
A;Reference number: S61072
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73; Conserv
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631, 1994
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Pred. No. 0.
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M1 protein precursor - Streptococcus py C:Species: Streptococcus pyogenes C:Date: 19-Mar-1997 #sequence_revision C:Accession: S46489; S46490 R:Akesson, P: Schmidt, K.H.; Cooney, J Biochem. J. 300, 877-886, 1994

Streptococcus pyogenes

Biochem. J. A; Title: M1

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streptococcal surface

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19-Mar-1997 #text_change

07-May-1999

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A; Reference number: $46489; MUI:
A; Accession: $46489
A; Molecule type: DNA
A; Residues: 1-494 <AKE>
A; Experimental source: strain 4-
A; Accession: $46490
A; Molecule type: protein
A; Residues: 42-51 <AKW>
A; Experimental source: strain 4-
A; Experimental source: strain 4-
                                                                                                                                                                                                                                                 RESULT 38
T14867
T14867
C:Species: Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T14867
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A;Gene: emml
C;Superfamily: M5 protein
C;Keywords: transmembrane protein
C;Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted
F;42-484/Product: M1 protein #status experimental
F;459-477/Domain: transmembrane #status predicted
                                                A; Gene: ab
A; Introns:
                                                                             A;Cross-references:
C;Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                           A; Reference number: Z18248; MUID: 98365468 A; Accession: T14867
                                                                                                                                                                                                                     R;Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, J. Cell Biol. 142, 735-750, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPDEELVGAFPI 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QA-SQDYNRANVLEKELETITREQEINRNLLGNAKLELDQLSSEKEQLTIEKAKLEEEKQ
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Similarity 21.6%;
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                                                                                                                                                                                                    an actin-binding protein
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   .0%;
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Pred. No. 0.086;
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                                                                                          NID: g3549260; PID: g3549261; PIDN: AAC34582
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1935 <KOl>
A;Cross-references: GB:U75316; NID:g1698894; PIDN:AAB37320.1; PID:g1698895
A;Cross-references: strain domestica
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: cardiac muscle; heart
C;Keywords: cardiac muscle; heart
F;88-766/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myosin heavy chain beta chain, cardiac - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000
C:Accession: A59286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A59286
A; Accession: A59286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A59286
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  289
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                                                                                                                                                                                                                                                                                                                                                                              79
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DRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSP 348
                                              KQKYEE----SQSELESSQKEARSLSTELFKLKNAYEESLEHLETSKRENKNLQEEISDLT
                                                                                        QTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKL--
                                                                                                                                                                                       MGVGQSAVEQLAVYCVSLKK-----EYENLK---EARKASGEVADKLRKDLFSSRSKL
                                                                                                                                                                                                                                     YEEETETKAELQRVLSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEE----
                                                                                                                                                                                                                                                                                 LKKQMKYLEQQQDETKQAQEEAGRLRSKMKT.....MEQIELLLQSQLPEVEEMIRD
                                                                                                                                                                                                                                                                                                                              LSRQLDEKEALISQLTRGKLTYTQQLEDLKRQLEEEVKAKNALAHALQSARHAADLLREQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRK-----DLFSSRSKLQTVYSEL
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                                                                                                                                        ----AVEAVNAKCSSLEKTKHRLQNEIEDLMVDVERSNAAAAALDKKQRNFDKILAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRPNQIEIDRLVNEIVNRNQDLIRK-----NKTKF 1651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQP 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLLKEKLKPLELDSNEKQKTIDDLLSNISNLQISLQNDKDLISERNNSIKTLESRITQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 166; DB Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                          TMLOETLNLPPVASETV 288
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19;

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bullous pemphigoid antigen 1 precursor - human
N;Alternate names: 230k bullous pemphigoid autoantigen; BP230 antigen
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 11-Jul-1997 #text_change 21-Jul-2000
C;Accession: I56317; A40937; A40882; A61393; A37342; S46669
R;Elgart, G.W.; Stanley, J.R.
J. Invest. Dermatol. 101, 244-246, 1993
A;Title: Cloning of the 5' mRNA for the 230-kD bullous pemphigoid antigen by A;Reference number: I56317; MUID:93346806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Note: the sequence from Fig. 3 is inconsistent with the nucleotide sequence R:Owaribe, K.; Kartenbeck, J.; Stumpp, S.; Magin, T.M.; Krieg, T.; Diaz, L.A Differentiation 45, 207-220, 1990
A:Title: The hemidesmosomal plaque. Characterization of a major constituent A:Reference number: A37342; MUID:91216368
A:Accession: A37342
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A40937
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A;Title: Bullous pemphigoid antigen: cDNA cloning, cellular eA;Reference number: A61393; MUID:91258872
A;Accession: A61393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M69225
R;Tanaka, T.; Parry, D.A.D.; Klaus-Kovtun, V.; Steinert, P.M.; Stanley, J.R.
J. Biol. Chem. 266, 12555-12559, 1991
A;Title: Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I
A;Reference number: A40882; MUID:91286285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Human bullous pemphigoid antigen (BPAG1). Amino acid sequences deduced A;Reference number: A40937; MUID:92011493 A:Accession: A40937
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                                                                                                                                                                                                                                                                                                                          R; Hopkinson, S.B.; Jones, J.C.R.
Biochem. J. 300, 851-857, 1994
A;Title: Identification of a second protein
A;Reference number: S46669; MUID:94280413
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1595-1942,'R',1944-2202 <OWA>
A;Cross-references: GB:X58677; NID:g36094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: mRNA
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                                                          A; Map position: 6
A; Introns: 2016/3
                                                                                                                  A;Gene: GDB:BPAG1
A;Cross-references:
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1897-2081 <HOP>
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A; Residues: 1722-2649 <SAW2>
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A; Residues: 1-850, 'G', 852-1643, 'T', 1645-2363, 'T', 2365-2494,'V', 2496-2542,'K', 2544-2649
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                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                       A; Accession: S46669
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A; Residues: 555-2649 <TAN>
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           Keywords:
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        list of introns is basement membrane;
                                                                                         6p12-6p11
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17784-17790, 1991
                                                                                                                  GDB:125207; OMIM:113810
                                                                                                                                                                                             EMBL: U04850;
not complete
extracellular matrix; glycoprotein; membrane
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                                                                                                                                                                                             NID:g451556;
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1742 EESGKF
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                                                                                            SKDVVRTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPS-----LFQ
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                                                              SKEEKRRGEQKVQLQQAQVQELNNRL-----
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